In the Claims

Please amend the claims as follows:

- 1-23. (Cancelled)
- (Currently amended) The method of claim 23, A method for identifying elite 24. event MS-B2 in a transgenic Brassica plant, or cell or tissue thereof, or transgenic Brassica plant material, said method comprising amplifying a DNA fragment of between 100 and 300 nucleotides 160 and 200 by from a nucleic acid present in said transgenic Brassica plant, or cell or tissue thereof, or transgenic *Brassica* plant material, using a polymerase chain reaction (PCR) with a first specific primer or probe at least two primers, one of which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in hybridizes to bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in to bases 194-416 of SEQ ID NO:10, or the complement thereof; of MS B2, and a second specific primer or probe the other of which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to hybridizes to a sequence within SEQ ID NO:1; and thus identifying a Brassica plant, or cell or tissue thereof, or transgenic plant material comprising elite event MS-B2, if said genomic DNA amplifies the DNA fragment using PCR with the primers and detecting said amplified DNA fragment on an agarose gel.
- 25. (Currently amended) The method of claim 24, wherein one of said second specific primer or probe primers hybridizes to a sequence within SEQ ID NO:1 and comprises the sequence of SEQ ID NO: 12.
- 26. (Currently amended) The method of claim 24, wherein one of said <u>first specific</u> primer or probe comprises at least 16 consecutive nucleotides from the 3' flanking region of MS-B2, comprised in primers hybridizes to bases 194-416 of SEQ ID NO:10, or the complement thereof and comprises the sequence of SEQ ID NO:11.
 - 27-29. (Cancelled)
- 30. (Currently amended) The kit of Claim 29, which further comprises at least A kit for identifying elite event MS-B2 in a transgenic Brassica plant, or cell or tissue thereof, or transgenic Brassica plant material, said kit comprising at least a first PCR primer or probe and a second PCR primer or probe, wherein the first PCR primer or probe comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ

00156136

ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof; and a second specific primer or probe which comprises at least 16 consecutive nucleotides from foreign DNA of MS-B2, or the complement thereof, said foreign DNA corresponding hybridizes-to a sequence within SEQ ID NO:1 of MS-B2.

- 31. (Currently amended) The kit of claim 30, wherein said <u>second at least one PCR</u> primer <u>or probe</u> comprises the sequence of SEQ ID NO:12.
- 32. (Currently amended) The kit of claim [[29]] 30, wherein said <u>first at least one</u> PCR primer or probe comprises the sequence of SEQ ID NO:11.
 - 33. (Cancelled)
- 34. (Currently amended) A method for screening the genomic DNA of seeds for the presence of MS-B2, which method comprises detecting, in the genomic DNA of seeds, an MS-B2 specific region comprising the insertion site of MS-B2, using a polymerase chain reaction with a first specific primer or probe which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in hybridizes to bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in to bases 194-416 of SEQ ID NO:10, or the complement thereof, of MS-B2, and a second specific primer or probe which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1; and thus confirming the presence of MS-B2 if the MS-B2 specific DNA sequence is so detected in said seeds samples of seed lots.
- 35. (Currently amended) A method for screening the genomic DNA of seeds for the absence of MS-B2, which method comprises carrying out, in the genomic DNA of seeds, a polymerase chain reaction Polymerase Chain Reaction or Southern Blot using a first specific primer or probe which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in hybridizes to bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in to bases 194-416 of SEQ ID NO:10, or the complement thereof; of MS-B2, and a second specific primer or probe which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1; and not detecting the

presence of MS-B2 specific DNA on an agarose gel or Southern Blot membrane, thus confirming the absence of MS-B2 in said seeds.

- 36. (Currently amended) A method for identifying a Brassica plant, or cell or tissue thereof, or Brassica plant material not comprising elite event MS-B2, which method comprises establishing whether the genomic DNA of the plant, or cell, or tissue thereof, or transgenic plant material cannot amplify a DNA fragment of between 100 and 300 nucleotides using performing a polymerase chain reaction (PCR) with a first primer or probe at least two primers, one of which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in recognizes bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof; of MS-B2, and a second specific primer or probe which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to another of which recognizes a sequence within SEQ ID NO:1; and thus identifying a Brassica plant, or cell or tissue thereof, or transgenic plant material not comprising elite event MS-B2, if said genomic DNA cannot amplify the DNA fragment using PCR with the primers, and detecting the absence of a DNA fragment of between 160 and 200 base pairs on an agarose gel.
- 37. (New) The method of claim 24, wherein said first specific primer or probe comprises 20 to 24 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof, and said second specific primer or probe comprises 20-24 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1.
- 38. (New) The method of claim 24, wherein said first specific primer or probe comprises the sequence of SEQ ID NO:11.
- 39. (New) The method of claim 24, wherein said first specific primer or probe comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ ID NO:8, or the complement thereof.
- 40. (New) The kit of claim 30, wherein said first PCR primer or probe comprises 20-24 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of

5 00156136

SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof, and wherein said second specific primer or probe comprises 20-24 consecutive nucleotides from foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1.

- 41, (New) The kit of claim 30, wherein said first PCR primer or probe comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ ID NO:8, or the complement thereof.
- 42. (New) The kit of claim 30, wherein said first PCR primer or probe comprises at least 16 consecutive nucleotides from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof.

6

00156136